Amendments to the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 23, lines 13-16 and replace it with the following paragraph:

- figures 4-1 to 4-3 illustrate a first example of steps a) to f) of the method according to the invention; figures 4-1: steps a and b **(SEQ ID NOS: 2-3 and 14)**, figure 4-2: steps c and d **(SEQ ID NOS: 14-17)**, figure 4-3: steps e and f **(SEQ ID NOS: 4-5, 15 and 18)**;

Please delete the paragraph on page 24, lines 21-24 and replace it with the following paragraph:

- figures 5-1 to 5-3 illustrate a second example of steps a) to f) of the method according to the invention: figure 5-1: steps a and b **(SEQ ID NOS: 2 and 19-20)**, figure 5-2: steps c and d **(SEQ ID NOS: 20-24)**, figure 5-3: steps e and f **(SEQ ID NOS: 4-5, 18, 21 and 25)**;

Please delete the paragraph on page 25, lines 29-32 and replace it with the following paragraph:

- figures 6-1 to 6-3 illustrate a third example of steps a) to f) of the method according to the invention: figure 6-1: steps a and b **(SEQ ID NOS: 2, 26-27 and 37)**, figure 6-2: steps c and d **(SEQ ID NOS: 27-30)**, figure 6-3: steps e and f **(SEQ ID NOS: 18, 28 and 31-32)**;

Please delete the paragraph on page 35, line 36 to page 27, line 9 and replace it with the following paragraph:

- figure 7 illustrates an example of implementation of the method according to the invention using two different exzymes E1 ($E1_A$ cleaves frequently, such as *Msp I* and *Taq*^{a} *I,* and $E1_C$ cleaves rarely, such as *Pst I, EcoR I*), so as to further reduce the complexity of the DNA to be analyzed, by introduction of an additional selection through cleavage with the enzyme $E1_C$. The sequences of the resection sites are indicated in the 5'→ 3' direction for the positive strand. The bases indicated in bold remain on the fragment of interest after cleavage. The bases underlined are those that are imposed by the coupling of the $E1_A$ and E2 enzymes **(SEQ ID NOS: 33-36, respectively in order of appearance)**;